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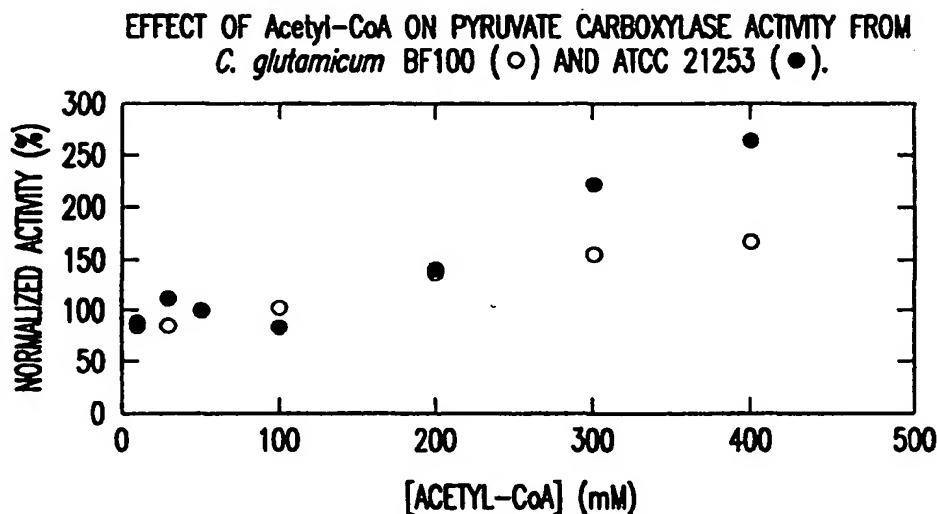
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(54) Title: **FEEDBACK-RESISTANT PYRUVATE CARBOXYLASE GENE FROM CORYNEBACTERIUM**



(57) Abstract: The present invention relates to a mutated pyruvate carboxylase gene from *Corynebacterium*. The mutant pyruvate carboxylase gene encodes a pyruvate carboxylase enzyme which is resistant to feedback inhibition from aspartic acid. The present invention also relates to a method of replacing the wild-type pyruvate carboxylase gene in *Corynebacterium* with this feedback-resistant pyruvate carboxylase gene. The present invention further relates to methods of the production of amino acids, preferably lysine, comprising the use of this mutant pyruvate carboxylase enzyme in microorganisms.



For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Feedback-Resistant Pyruvate Carboxylase Gene from *Corynebacterium*

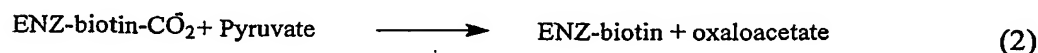
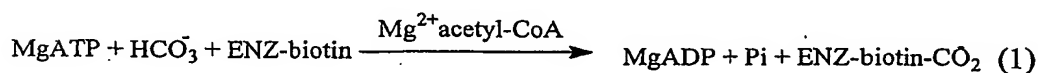
Background of the Invention

Field of the Invention

5 The present invention relates to a mutated pyruvate carboxylase gene from *Corynebacterium*. The mutant pyruvate carboxylase gene encodes a pyruvate carboxylase enzyme which is resistant to feedback inhibition from aspartic acid. The present invention also relates to a method of replacing the wild-type pyruvate carboxylase gene in *Corynebacterium* with this feedback-resistant pyruvate carboxylase gene. The present invention further relates to methods of the production of amino acids, preferably lysine, comprising the use of this mutant pyruvate carboxylase enzyme in microorganisms.

Background of the Invention

15 Pyruvate carboxylase is an important biotin-containing enzyme found in a variety of plants and animals, as well as some groups of bacteria (Modak, H.V. and Kelly, D.J., Microbiology 141:2619-2628 (1995)). In the presence of adenosine triphosphate (ATP) and magnesium ions, pyruvate carboxylase catalyzes the two-step carboxylation of pyruvate to form oxaloacetate, as shown in the equations below:



 In reaction (1) the ATP-dependent biotin carboxylase domain carboxylates a biotin prosthetic group linked to a specific lysine residue in the biotin-carboxyl-carrier protein (BCCP) domain. Acetyl-coenzyme A activates reaction (1) by

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increasing the rate of bicarbonate-dependent ATP cleavage. In reaction (2), the BCCP domain donates the CO₂ to pyruvate in a reaction catalyzed by the transcarboxylase domain (Attwood, P.V., *Int. J. Biochem. Cell. Biol.* 27:231-249 (1995)).

5 In bacteria such as *Corynebacterium glutamicum*, pyruvate carboxylase is utilized during carbohydrate metabolism to form oxaloacetate, which is in turn used in the biosynthesis of amino acids, particularly L-lysine and L-glutamate. Furthermore, in response to a cell's metabolic needs and internal environment, the activity of pyruvate carboxylase is subject to both positive and negative
10 feedback mechanisms, where the enzyme is activated by acetyl-CoA, and inhibited by aspartic acid. Based on its role in the pathway of amino acid synthesis, and its ability to be regulated, pyruvate carboxylase plays a vital role in the synthesis of amino acids.

Bacteria such as *C. glutamicum* and *E. coli* are widely used in industry for
15 the production of amino acids such as L-glutamate and L-lysine. Because of the central importance of pyruvate carboxylase in the production of amino acids, particularly L-glutamate and L-lysine, the exploitation of pyruvate carboxylase to increase amino acid production is of great interest in an industrial setting. Thus, promoting the positive feedback mechanism of pyruvate carboxylase, or
20 inhibiting its negative feedback mechanism, in *C. glutamicum* or could augment amino acid production on an industrial scale.

Summary of the Invention

One aspect of the present invention relates to a nucleic acid molecule comprising a nucleotide sequence which codes for a pyruvate carboxylase of SEQ
25 ID NO:19, wherein this pyruvate carboxylase contains at least one mutation which desensitizes the pyruvate carboxylase to feedback inhibition by aspartic acid.

Another aspect of the present invention provides methods for using the nucleic acid of SEQ ID NO:1 or SEQ ID NO:3, which encodes the amino acid sequence of a mutant pyruvate carboxylase. Such uses include the replacement of the wild-type pyruvate carboxylase with the feedback-resistant pyruvate carboxylase, and the production of amino acids. An additional aspect of the present invention provides a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4. Still another aspect of the present invention provides a polypeptide comprising the amino acid sequence selected from the group comprising SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12
10 SEQ ID NO:14, SEQ ID NO:16 and SEQ ID NO:18.

Another aspect of the present invention also relates to a nucleic acid molecule comprising a nucleotide sequence which encodes the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, or the amino acid sequence encoded by the DNA contained in Deposit Number NRRL B-11474. Another aspect of
15 the present invention further relates to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 and SEQ ID NO:3.

Brief Description of the Figures

Figures 1A-1E show the full-length nucleotide sequence (SEQ ID NO:1) encoding the amino acid sequence of feedback-resistant pyruvate carboxylase, and the corresponding amino acid sequence (SEQ ID NO:2).
20

Figure 2 shows the comparison of amino acid sequences between the wild-type pyruvate carboxylase, isolated from ATCC21253, and the feedback-resistant pyruvate carboxylase (SEQ ID NO:2), isolated from Deposit Number NRRL B-11474.

Figures 3A-3B show the full-length nucleotide sequence (SEQ ID NO:3) encoding the amino acid sequence of feedback-resistant pyruvate carboxylase.
25

Figure 4 shows the effects of various substrate concentrations on the pyruvate carboxylase activity in *C. glutamicum* ATCC 21253 and NRRL B-11474.

Figure 5 shows the effects of aspartate concentration on the activity of pyruvate carboxylase in *C. glutamicum* ATCC21253 and NRRL B-11474.

5 *Figure 6* shows the effects of acetyl-CoA concentration on the activity of pyruvate carboxylase in *C. glutamicum* ATCC21253 and NRRL B-11474.

Detailed Description of the Preferred Embodiments

The present invention relates to variations of the polypeptide comprising the amino acid sequence which codes for the pyruvate carboxylase as shown in
10 SEQ ID NO:19. Preferably, the variations of pyruvate carboxylase enzyme in the present invention contain at least one mutation which desensitizes the pyruvate carboxylase to feedback inhibition by aspartic acid. Such mutations may include deletions, insertions, inversions, repeats, and type substitutions. More preferably, the amino acid sequence mutation which desensitizes the wild-type pyruvate
15 carboxylase enzyme (SEQ ID NO:19) to feedback inhibition comprises at least one substitution selected from the group consisting of (a) methionine at position 1 being replaced with a valine, (b) glutamic acid at position 153 being replaced with an aspartic acid, (c) alanine at position 182 being replaced with a serine, (d) alanine at position 206 being replaced with a serine, (e) histidine at position
20 227 being replaced with an arginine, (f) alanine at position 452 being replaced with a glycine, and (g) aspartic acid at position 1120 being replaced with a glutamic acid. Still more preferably, the variation of the polypeptide encoded by the amino acid sequence of SEQ ID NO:19 contains more than one of the above-mentioned mutations. Most preferably, the variation of the polypeptide encoded
25 by the amino acid sequence of SEQ ID NO:19 contains all of the above-mentioned mutations. As one of ordinary skill in the art would appreciate, the numbering of amino acid residues of a protein as used herein, begins at the amino

terminus (N-terminus) and proceeds towards the carboxy terminus (C-terminus), such that the first amino acid at the N-terminus is position 1.

An embodiment of the present invention relates to an isolated or purified nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence which encodes the amino acid sequence of SEQ ID NO:2, (b) a nucleotide sequence which encodes the amino acid sequence of SEQ ID NO:4, (c) a nucleotide sequence encoding the amino acid sequence encoded by the DNA contained in Deposit Number NRRL B-11474 or (d) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), or (c).

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 97%, 98%, 99% or 100% identical, to any of the nucleotide sequences in (a), (b), (c) or (d) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a), (b), (c) or (d) above. However, the polynucleotide which hybridizes does not hybridize under stringent hybridization conditions to a polynucleotide having a nucleotide sequence consisting of only A residues or of only T residues.

Another aspect of the invention is directed to nucleic acid molecules at least 90%, 95%, 97%, 98% or 99% identical to the nucleic acid sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3) or to the nucleic acid sequence of the deposited DNA (NRRL B-30293, deposited May 30, 2000).

A further aspect of the invention provides a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 and SEQ ID NO:17.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that

the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the pyruvate carboxylase polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence.

As a practical matter, whether any particular nucleic acid molecule is at least 90%, 95%, 97%, 98% or 99% identical to, for instance, the nucleotide sequence shown in Figure 1 or to the nucleotide sequence of the deposited DNA can be determined conventionally using known computer programs such as the FastA program. FastA performs a Pearson and Lipman search for similarity between a query sequence and a group of sequences of the same type nucleic acid. Professor William Pearson of the University of Virginia Department of Biochemistry wrote the FASTA program family (FastA, TFastA, FastX, TFastX and SSearch). In collaboration with Dr. Pearson, the programs were modified and documented for distribution with GCG Version 6.1 by Mary Schultz and Irv Edelman, and for Versions 8 through 10 by Sue Olson.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the ABI Prism 377). Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule.

Unless otherwise indicated, each "nucleotide sequence" set forth herein is presented as a sequence of deoxyribonucleotides (abbreviated A, G, C and T). However, by "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of

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deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U) where each thymidine deoxynucleotide (T) in the specified deoxynucleotide sequence is replaced by the ribonucleotide uridine (U). For instance, reference to an RNA molecule
5 having the sequence of SEQ ID NO:1 set forth using deoxyribonucleotide abbreviations is intended to indicate an RNA molecule having a sequence in which each deoxynucleotide A, G or C of SEQ ID NO:1 has been replaced by the corresponding ribonucleotide A, G or C, and each deoxynucleotide T has been replaced by a ribonucleotide U.

10 As indicated, nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, DNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-
15 coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated
20 DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

25 In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described herein. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC
30 (150 mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x

Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C. By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide (e.g., the deposited plasmid), for instance, a portion 25-750 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of the nucleotide sequences of any of the nucleotide sequences included in the present invention. By a portion of a polynucleotide of "at least 20 nt in length," for example, is intended 20 or more contiguous nucleotides from any of the nucleotide sequences of the reference polynucleotides, (e.g., the deposited DNA or the nucleotide sequence as shown in any of the figures). As indicated, such portions are useful diagnostically either as a probe, according to conventional DNA hybridization techniques, or as primers for amplification of a target sequence by the polymerase chain reaction (PCR), as described, for instance, in *Molecular Cloning, A Laboratory Manual*, 2nd. edition, edited by Sambrook, J., Fritsch, E. F. and Maniatis, T., (1989), Cold Spring Harbor Laboratory Press, the entire disclosure of which is hereby incorporated herein by reference.

The nucleic acid molecules of the present invention are suitable for use in vectors. As such, polynucleotides of interest can be joined to the nucleic acid molecules of the present invention, which may optionally contain selectable markers. A preferred embodiment of the present invention is that the vector comprises a functional *Corynebacterium* replication origin. A replication origin is a nucleotide sequence, typically several hundred base pairs long, that is vital to the initiation of DNA replication.

The vectors can optionally contain an exogenous terminator of transcription; an exogenous promoter; and a discrete series of restriction endonuclease recognition sites, said series being between said promoter and said terminator. The vector can optionally contain their native expression vectors
5 and/or expression vectors which include chromosomal-, and episomal-derived vectors, e.g., vectors derived from bacterial exogenous plasmids, bacteriophage, and vectors derived from combinations thereof, such as cosmids and phagemids.

A DNA insert of interest should be operatively linked to an appropriate promoter, such as its native promoter or a host-derived promoter, the phage
10 lambda P_L promoter, the phage lambda P_R promoter, the *E. coli lac* promoters, such as the *lacI* and *lacZ* promoters, *trp* and *tac* promoters, the T3 and T7 promoters and the *gpt* promoter to name a few. Other suitable promoters will be known to the skilled artisan.

The expression constructs will further contain sites for transcription
15 initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs can include a translation initiating codon at the beginning and a termination codon appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one
20 selectable marker. Preferably the selection marker comprises a nucleotide sequence which confers antibiotic resistance in a host cell population. Such markers include amikacin, augmentin (amoxicillin plus clavulonic acid), ampicillin, cefazolin, cefoxitin, ceftazidime, ceftiofur, cephalothin, enrofloxacin,
25 florfenicol, gentamicin, imipenem, kanamycin, penicillin, sarafloxacin, spectinomycin, streptomycin, tetracycline, ticarcillin, tilmicosin, or chloramphenicol resistance genes. Other suitable markers will be readily apparent to the skilled artisan.

The invention also provides for a method of producing a host cell where
30 the expression vectors of the current invention have been introduced into the host

cell. Methods of introducing genetic material into host cells, such as those described in typical molecular biology laboratory manuals, for example J. Sambrook, E.F. Fritsch and T. Maniatis, *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), are well known to the skilled artisan. These methods include, but are not limited to, calcium phosphate transfection, DEAE-dextran mediated transfection, microinjection, lipid-mediated transfection, electroporation or infection. Accordingly, a preferred embodiment of the present invention provides a host cell comprising the vector of the present invention.

As used in the present invention, a host cell refers to any prokaryotic or eukaryotic cell where the desired nucleic acid sequence has been introduced into the cell. There are a variety of suitable host cells, including but not limited to bacterial, fungal, insect, mammalian and plant cells, that can be utilized in the present invention. Representative bacterial host cells include, but are not limited to, *Streptococci*, *Staphylococci*, *E. coli*, *Streptomyces*, *Bacillus* and *Corynebacterium*. Representative fungal cells include but are not limited to, yeast cells and *Aspergillus*. Insect cells include, but are not limited to, *Drosophila* S2 and *Spodoptera* Sf9 cells. Examples of mammalian cells include, but are not limited to, CHO, COS and Hela cells.

The present invention provides methods for utilizing the nucleic acid of SEQ ID NO:1 or SEQ ID NO:3, which encodes the amino acid sequence of a mutant pyruvate carboxylase. Such methods include the replacement of the wild-type pyruvate carboxylase with the feedback-resistant pyruvate carboxylase, and the production of amino acids. The method for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a *Corynebacterium glutamicum* host cell comprises the steps of: (a) replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombinant strain; and (b) replacing the selectable marker gene of step (a) in the first recombinant strain, with the feedback resistant pyruvate carboxylase gene through

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homologous recombination to form a second recombinant strain. The homologous recombination in steps (a) and (b) would occur between the genetic material of the host cell and any of the vectors of the present invention.

Homologous recombination is a technique that is used to disrupt
5 endogenous nucleotide sequences in a host cell. Normally, when an exogenous nucleotide sequence is inserted into a host cell, this polynucleotide may randomly insert into any area of the host cell's genome, including endogenous plasmids. However, with homologous recombination, the exogenous nucleotide sequence contains sequences that are homologous to an endogenous nucleotide sequence
10 within the host cell. Once introduced into the cell, for example by electroporation, the exogenous nucleotide sequence will preferentially recombine with and replace the endogenous nucleotide sequence with which it is homologous.

As used herein, an exogenous nucleotide sequence, is a nucleotide
15 sequence which is not found in the host cell. Thus, the term exogenous nucleotide sequence is meant to encompass a nucleotide sequence that is foreign to the host cell, as well as a nucleotide sequence endogenous, or native, to the host cell that has been modified. Modification of the endogenous nucleotide sequence may include, for instance, mutation of the native nucleotide sequence
20 or any of its regulatory elements. As used herein, mutation is defined as any change in the wild-type sequence of the host's genetic material, including plasmid DNA. An additional form of modification may also include fusion of the endogenous nucleotide sequence to a nucleotide sequence that is normally not present, in relation to the endogenous nucleotide sequence.

25 Host cells that have undergone homologous recombination are selected on the basis of antibiotic resistance through the use of, for example, the selectable markers mentioned above. The process of selecting cells that have undergone homologous recombination will be readily apparent to one skilled in the art.

Another aspect of the current invention is a method for producing amino
30 acids. In the current context, production of amino acids is accomplished by

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culturing host cells where a vector of the present invention has been introduced into the host cell, or culturing host cells where homologous recombination, involving a vector of the present invention, has taken place. Culturing of the host cells is performed in the appropriate culture media. Subsequent to culturing the host cells in culture media, the desired amino acids are separated from the culture media. Preferably, the amino acids produced by the methods described herein include L-lysine, L-threonine, L-methionine, L-isoleucine, L-glutamate, L-arginine and L-proline. More preferably, the present invention relates to the production of L-lysine.

The present invention provides an isolated or purified polypeptide encoded by the DNA plasmid encoding pyruvate carboxylase contained in Deposit Number NRRL B-30293, the amino acid sequence of SEQ ID NO:2 or the amino acid sequence of SEQ ID NO:4. Still another aspect of the present invention provides a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 and SEQ ID NO:18.

Accordingly, SEQ ID NO:6 corresponds to the amino acid sequence: PSKNIDDIVKSAE. SEQ ID NO:8 corresponds to the amino acid sequence: RGMRFVSSPDELRL. SEQ ID NO:10 corresponds to the amino acid sequence: AAFGDGGSVYVERA. SEQ ID NO:12 corresponds to the amino acid sequence: VQILGDRTGEVVH. SEQ ID NO:14 corresponds to the amino acid sequence: IATGFIGDHPHLL. SEQ ID NO:16 corresponds to the amino acid sequence: TITASVEGKIDRV. SEQ ID NO:18 corresponds to the amino acid sequence: MTAITLGGLLLKGITLV.

All of the polypeptides of the present invention are preferably provided in an isolated form. As used herein, "isolated polypeptide" is intended to mean a polypeptide removed from its native environment. Thus, a polypeptide produced and/or contained within a recombinant host cell is considered isolated for purposes of the present invention. Also intended as an "isolated polypeptide" are polypeptides that have been purified, partially or substantially, from a

recombinant host. For example, a recombinantly produced version of the pyruvate carboxylase enzyme can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988).

One aspect of the present invention include the polypeptides which are at least 80% identical, more preferably at least 90%, 95% or 100% identical to the polypeptide encoded by the DNA plasmid encoding pyruvate carboxylase contained in Deposit Number NRRL B-30293, the polypeptide of SEQ ID NO:2 or the polypeptide of SEQ ID NO:4.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to the amino acid sequence of SEQ ID NO:2, for example, it is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the amino acid sequence of SEQ ID NO:2, for example. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is, for instance, 95% identical to the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:4 or to the amino acid sequence encoded by deposited DNA clone can be determined conventionally using known computer programs such the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). When using Bestfit or any other sequence alignment program to

determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set, of course, such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed.

Another aspect of the present invention provides a nucleic acid molecule encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 and SEQ ID NO:18. Preferably, the invention provides for nucleic acid molecules, which code for the aforementioned polypeptides, that are selected from the group consisting of SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 and SEQ ID NO:17.

Accordingly, SEQ ID NO:5 corresponds to the nucleic acid sequence that codes for the amino acid sequence of SEQ ID NO:6. SEQ ID NO:7 corresponds to the nucleic acid sequence that codes for the amino acid sequence of SEQ ID NO:8. SEQ ID NO:9 corresponds to the nucleic acid sequence that codes for the amino acid sequence of SEQ ID NO:10. SEQ ID NO:11 corresponds to the nucleic acid sequence that codes for the amino acid sequence of SEQ ID NO:12. SEQ ID NO:13 corresponds to the nucleic acid sequence that codes for the amino acid sequence of SEQ ID NO:14. SEQ ID NO:15 corresponds to the nucleic acid sequence that codes for the amino acid sequence of SEQ ID NO:16. SEQ ID NO:17 corresponds to the nucleic acid sequence that codes for the amino acid sequence of SEQ ID NO:18.

Methods used and described herein are well known in the art and are more particularly described, for example, in J.H. Miller, *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1972); J.H. Miller, *A Short Course in Bacterial Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1992); M. Singer and P. Berg, *Genes & Genomes*, University Science Books, Mill Valley, California (1991); J.

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Examples

The following examples are illustrative only and are not intended to limit the scope of the invention as defined by the appended claims.

Strains and Media

5 Bacterial strains used were *Corynebacterium glutamicum* ATCC 21253 and NRRL B-11474. These strains have an auxotrophy for homoserine (ATCC 21253) and for threonine, methionine and alanine (NRRL B-11474).

10 Defined medium for *Corynebacterium glutamicum* ATCC 21253 contained the following ingredients (per liter): glucose, 20 g; NaCl, 2 g; citrate (trisodium salt, dihydrate), 3 g; $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 0.1 g; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.5 g; $\text{Na}_2\text{EDTA} \cdot 2\text{H}_2\text{O}$, 75 mg; $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 50 mg; 100x salt solution, 20 ml; K_2HPO_4 , 4 g; KH_2PO_4 , 2 g; $(\text{NH}_4)_2\text{SO}_4$, 7.5 g; urea, 3.75 g; leucine, 0.1 g; threonine, 0.15 g; methionine, 0.05 g; thiamine, 0.45 mg; biotin, 0.45 mg; pantothenic acid, 4.5 mg (pH 7.0). The salt solution contained the following
15 ingredients (per liter): MnSO_4 , 200 mg; $\text{Na}_2\text{B}_4\text{O}_7 \cdot 10\text{H}_2\text{O}$, 20 mg; $(\text{NH}_4)_6\text{Mo}_7\text{O}_{24} \cdot 4\text{H}_2\text{O}$, 10 mg; $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$, 200 mg; $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 50 mg; $\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$, 20 mg (pH 2.0).

20 Defined medium for *Corynebacterium glutamicum* NRRL B-11474 contained the following ingredients (per liter): glucose, 20 g; NaCl, 1 g; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.4 g; $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.01 g; $\text{MnSO}_4 \cdot \text{H}_2\text{O}$, 0.01 g; KH_2PO_4 , 1 g; $(\text{NH}_4)_2\text{SO}_4$, 10 g; urea, 2.5 g; alanine, 0.5 g; threonine, 0.25 g; methionine, 0.5 g; thiamine, 0.45 mg; biotin, 0.45 mg; niacinamide, 50 mg (pH 7.2).

Pyruvate Carboxylase and Phosphoenol Pyruvate Carboxylase Assay

25 Pyruvate carboxylate and phosphoenol pyruvate carboxylate assays were performed with permeabilized cells prepared by the following method. Log phase cells were harvested by centrifugation for 10 min at 5000 xg at 4°C and washed with 20 ml of the ice-cold washing buffer (50 mM Tris/HCl [pH 6.3] containing

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50 mM NaCl). The cell pellet was resuspended in an ice-cold Hepes buffer (100 mM Hepes [pH 7.5] containing 20% Glycerol) to reach a final concentration of 25 g dry cell weight/liter. Resuspended cells were permeabilized by adding 30 μ l of a 10% Hexadecyltrimethyl-ammonium bromide (CTAB) (w/v) solution to 1 ml of cells to give a final concentration of 0.3% (CTAB)(v/v).

For determination of pyruvate carboxylate activity, the assay mixture contained 10 mM pyruvic acid, 14 mM KHCO_3 , 4 mM MgCl_2 , 1.75 mM ATP, 50 μ mole acetyl-CoA, 0.3 mg bovine serum albumin, 0.055 U citrate synthase and 50 mM sodium phosphate buffer ([pH 7.5] containing 0.1 mg 5, 5'-Dithio-bis(2-nitrobenzoic acid) (DTNB)) in a final volume of 1 ml. The reaction was started at 30°C with the addition of 10 μ l of the permeabilized cell suspension, and the formation of DTNB-thiophenolate was followed over time at 412 nm. Relevant standards and controls were carried out in the same manner.

For determination of phosphoenol pyruvate carboxylase activity, the assay mixture contained 10 mM phosphoenol pyruvate, 14 mM KHCO_3 , 4 mM MgCl_2 , 50 μ mole acetyl-CoA, 0.3 mg bovine serum albumin, 0.055 U citrate synthase and 50 mM sodium phosphate buffer ([pH 7.5] containing 0.1 mg 5, 5'-Dithio-bis(2-nitrobenzoic acid) (DTNB)) in a final volume of 1 ml. The reaction was carried out in the same conditions described for the pyruvate carboxylase assay.

The reproducibility for enzyme assays was typically 10%.

DNA Isolation and Purification

DNA was isolated from cultures of NRRL B-11474 cells. Defined media for NRRL B-11474 (CM media) contain the following ingredients, per liter: sucrose, 50 g; KH_2PO_4 , 0.5 g; K_2HPO_4 , 1.5 g; urea, 3 g; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.5 g; polypeptone, 20 g; beef extract, 5 g; biotin, 12.5 ml (60 mg/L); thiamine, 25 ml (120 mg/L); niacinamide, 25 ml (5g/L); L-methionine, 0.5 g; L-threonine, 0.25 g; L-alanine, 0.5 g. NRRL B-11474 cells were harvested from CM media and suspended in 10 ml of TE, pH 8 (10 mM Tris*Cl, 1 mM EDTA). Forty

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micrograms of RNase A and 10 milligrams of lysozyme were added per milliliter of suspension and the suspension was incubated at 37°C for 30 minutes. The suspension was made in 1.0% in sodiumdodecyl sulfate (SDS) and 0.1 mg/l proteinase K was added, and the cells were lysed by incubation at 37°C for 10 minutes. Nucleic acids were purified by three extractions with TE-saturated phenol (pH7), followed by ethanol precipitation. Nucleic acid precipitates were twice washed with 80% ethanol and redissolved in TE pH 8.

The concentrations of DNA were quantified spectrophotometrically at 260 nm. Purity of DNA preparations were determined spectrophotometrically (A260/A280 and A260/A230 ratios) and by agarose gel electrophoresis (0.8% agarose in 1x TAE).

Sequencing of the genomic DNA was performed, as is known by one of ordinary skill in the art, by creating libraries of plasmids and cosmids using pGEM3 and Lorist 6 respectively. Briefly, a Sau3AI digestion was performed on the genomic DNA and inserted into the BamHI site of pGEM3. The forward primer was used to generate a sequence, and primer walking generated the remainder of the sequence.

Activity of Pyruvate Carboxylase

Development of a Continuous Assay for Determining Pyruvate Carboxylase Activity

A discontinuous assay for determining pyruvate carboxylase from permeabilized cells has been previously described (Peters-Wendisch, P.G. *et al. Microbiology*, 143:1095-1103 (1997)). Because of the central location of OAA in the metabolism, it seemed to be that OAA would accumulate during the first reaction of the discontinuous assay. Most likely, OAA would be lost to other products, because of the competing enzymes that are still active. This depletion of OAA would inevitably lead to the underestimation of pyruvate carboxylase activity. To verify this assumption of decreasing OAA concentrations, a known

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amount of OAA was added to the first reaction in presence of permeabilized and non-permeabilized cells. A significant loss of OAA was detected, demonstrating that permeabilized cells are capable of further transformation of OAA.

To account for the intrinsic loss of OAA during the experiment, a continuous assay was carried out by coupling the two-reaction assay to a one-reaction assay in presence of an excess of citrate synthase. The amount of permeabilized cells added in the assay was optimized to obtain a detectable activity, with the lowest possible background absorbency due to the presence of cells.

To confirm that the continuous assay specifically detected pyruvate carboxylase activity, controls were carried out by assaying for activity in absence of each reaction component (Table 1). Using these controls, the detected activity was determined to be a carboxylation reaction requiring pyruvate, Mg and ATP.

Table 1: Controls for the continuous pyruvate carboxylate assay.

| Control | Detected Activity (Abs/min.mg DCW) |
|---------------------------|---------------------------------------|
| Complete mixture | 0.30 |
| Cells omitted | 0 |
| Pyruvate omitted | 0.01 |
| KHCO ₃ omitted | 0.03 |
| MgCl ₂ omitted | 0.02 |
| ATP omitted | 0.03 |
| Citrate synthase omitted | 0.10 |
| Complete + biotin | 0.35 |
| Complete + avidin | Not determined yet |

To optimize the assay, the influence of the ratio of CTAB:cells was tested. Maximal activity was measured between 8 and 24 mg CTAB/mg dry cell weight (DCW). Pyruvate carboxylase activity was measured in cells incubated with CTAB with varying incubation times. The activity of pyruvate carboxylase remained constant within 0 and 5 minutes. Similarly, different concentrations of DTNB, within the range 0.1-0.3 g/l, gave identical pyruvate carboxylase activity.

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To confirm the ability of the assay for determining pyruvate carboxylase activity in *Corynebacterium glutamicum*, different quantities of cells were used. Linearity between enzyme activity and quantity of cells was observed within the range 0-0.3 mg DCW.

5 *Enzymology Study of Pyruvate Carboxylase from Corynebacterium glutamicum:
Behavior of Pyruvate Carboxylase Towards Its Substrates*

Pyruvate carboxylase activity was determined as a function of various concentrations of its substrates: pyruvate, bicarbonate and ATP (Figure 4). Based on the data generated, the affinity constants of pyruvate carboxylase for its substrates were determined (Table 2). The pyruvate carboxylase from NRRL B-11474 and ATCC 21253 strains demonstrated a similar affinity for pyruvate and ATP. Pyruvate carboxylase activity in both strains were inhibited by ATP above a concentration of 2 mM. However pyruvate carboxylase in ATCC 21253 had a higher affinity for bicarbonate than pyruvate carboxylase from NRRL B-11474.

| Strain | $K_{M(\text{pyruvate})}$ [mM] | $K_{M(\text{HCO}_3^-)}$ [mM] | $K_{M(\text{ATP})}$ [mM] |
|----------------------|-------------------------------|------------------------------|--------------------------|
| <i>C. glutamicum</i> | | | |
| Pyc BF100 | 1.3 ± 0.3 | 14.4 ± 4 | 0.4 ± 0.1 |
| Pyc ATCC 21253 | 0.3 ± 0.1 | 2.9 ± 0.8 | 0.3 ± 0.1 |

Table 2: Comparison of affinity constants for substrates on pyruvate carboxylase from *C. glutamicum*, BF100 and ATCC 21253.

Aspartate Inhibition of Pyruvate Carboxylase

Aspartate inhibits phosphoenol pyruvate carboxylase (PEPC) activity. To determine the effect of aspartate on the activity of pyruvate carboxylase, aspartate was added at different concentrations in the spectrophotometer cuvette and

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enzyme activities were measured. As a comparison, the same experiment was carried out with PEPC in ATCC 21253 (Figure 5).

The PEPC of *Corynebacterium glutamicum* (ATCC 21253) was found to be strongly inhibited by aspartate. The enzyme was completely inhibited with a concentration of 5 mM aspartate. However, pyruvate carboxylase from the same strain was less sensitive to aspartate, i.e. it retained 35% of its original activity in the presence of 25 mM aspartate.

The pyruvate carboxylase activity in NRRL B-11474 showed a higher basal pyruvate carboxylase activity than ATCC 21253, i.e. the pyruvate carboxylase activity was about 5-times higher in NRRL B-11474 than in the ATCC 21253. Moreover, a dramatic difference in their aspartate inhibition patterns was found. Pyruvate carboxylase from NRRL B-11474 strain was activated by low aspartate concentrations within the range 0-30 mM and inhibited within the range 30-100 mM aspartate. Nevertheless it retained 50% of its original activity, even in the presence of 100 mM aspartate. Activity was maintained at 30% in the presence of 500 mM aspartate. On the other hand, Pyruvate carboxylase from ATCC 21253 was found to be more sensitive to aspartate than pyruvate carboxylase from NRRL B-11474. The pyruvate carboxylase from ATCC21253 lost 70% of its original activity at a concentration of 30 mM aspartame.

Activation of Pyruvate Carboxylase by Acetyl-CoA

Pyruvate carboxylase activity was measured in the presence of different concentrations of acetyl-CoA (Figure 6). Pyruvate carboxylase activity in both strains increased with increasing acetyl-CoA concentrations. The effect of acetyl-CoA on citrate synthase itself was studied also. Acetyl-CoA had a K_m of 10 μ M, demonstrating that under our conditions, citrate synthase is saturated with acetyl-CoA. Therefore, the increasing activity of pyruvate carboxylase with increasing

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acetyl-CoA concentration is the result of acetyl-CoA activating pyruvate carboxylase.

* * * * *

5 All publications mentioned herein above are hereby incorporated in their entirety by reference.

10 While the foregoing invention has been described in some detail for purposes of clarity and understanding, it will be appreciated by one skilled in the art from a reading of this disclosure that various changes in form and detail can be made without departing from the true scope of the invention and appended claims.

What Is Claimed Is:

1. An isolated or purified nucleic acid molecule comprising a nucleotide sequence which codes for a pyruvate carboxylase enzyme of SEQ ID NO:19, wherein said pyruvate carboxylase enzyme contains at least one mutation which
5 desensitizes said pyruvate carboxylase enzyme to feedback inhibition by aspartic acid selected from the group consisting of:

- (a) methionine at position 1 is replaced with a valine,
- (b) glutamic acid at position 153 is replaced with an aspartic acid,
- (c) alanine at position 182 is replaced with a serine,
- 10 (d) alanine at position 206 is replaced with a serine,
- (e) histidine at position 227 is replaced with an arginine,
- (f) alanine at position 452 is replaced with a glycine, and
- (g) aspartic acid at position 1120 is replaced with a glutamic acid.

2. An isolated or purified nucleic acid molecule comprising a nucleotide
15 sequence selected from the group consisting of:

- (a) the nucleotide sequence encoding amino acids 1 to 1157 of SEQ ID NO:2;
- (b) the nucleotide sequence encoding amino acids 1 to 1140 of SEQ ID NO:4;
- 20 (c) a nucleotide sequence encoding the amino acid sequence encoded by the DNA contained in Deposit Number NRRL B-30293; and
- (d) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b) or (c).

3. The nucleic acid molecule of claim 2, comprising the nucleotide sequence
25 of SEQ ID NO:1.

4. The nucleic acid molecule of claim 2, comprising the nucleotide sequence of SEQ ID NO:3.

5. A vector comprising:

- (a) the nucleic acid molecule of claim 1 or 2; and
- (b) at least one marker gene.

6. The vector of claim 5, further comprising a functional *Corynebacterium* replication origin.

7. A method for producing a host cell comprising introducing the vector of claim 5 into a host cell.

8. A host cell comprising the vector of claim 5.

9. A method of producing an amino acid, comprising:

- (a) culturing the host cell of claim 8, in a suitable media; and
- (b) separating said amino acid from said medium.

10. The method of claim 9, wherein said amino acid is selected from the group consisting of: L-lysine, L-threonine, L-methionine, L-isoleucine, L-glutamic acid, L-arginine and L-proline.

11. The method of claim 10, wherein said amino acid is L-lysine.

12. A method for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a *Corynebacterium glutamicum* host cell comprising the steps of:

(a) replacing a genomic copy of said wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombinant strain; and

(b) replacing said selectable marker gene of step (a) in said first recombinant strain, with said feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain;

wherein said homologous recombination in steps (a) and (b) occurs between said host cell and the vector of claim 5.

13. A host cell produced by the method of claim 12.

14. A method of producing an amino acid, comprising:

- (a) culturing the host cell of claim 13 in a suitable medium; and
- (b) separating said amino acid from said medium.

15. The method of claim 14, wherein said amino acid is selected from the group consisting of: L-lysine, L-threonine, L-methionine, L-isoleucine, L-glutamic acid, L-arginine and L-proline.

16. The method of claim 15, wherein said amino acid is L-lysine.

17. An isolated or purified polypeptide comprising the amino acid sequence of the polypeptide encoded by the DNA plasmid encoding pyruvate carboxylase contained in Deposit Number NRRL B-11474, the amino acid sequence of SEQ ID NO:2 or the amino acid sequence of SEQ ID NO:4.

18. An isolated or purified polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16 and SEQ ID NO:18.

19. An isolated or purified nucleic acid molecule comprising a nucleotide sequence encoding the polypeptide of claim 18.

20. The nucleic acid molecule of claim 19, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 and SEQ ID NO:17.

5

GTGACTGCTATCACCTTGGCGGTCTCTTGTGAAAGGAATAATTACTCTAGTGTCTGACT
1 -----+-----+-----+-----+-----+-----+-----+ 60
M T A I T L G G L L L K G I I T L V S T
CACACATCTTCAACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGGCGAAATC
61 -----+-----+-----+-----+-----+-----+-----+ 120
H T S S T L P A F K K I L V A N R G E I
GCGGTCCGTGCTTTCCGTGCAGCACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCC
121 -----+-----+-----+-----+-----+-----+-----+ 180
A V R A F R A A L E T G A A T V A I Y P
CGTGAAGATCGGGGATCATTCACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACT
181 -----+-----+-----+-----+-----+-----+-----+ 240
R E D R G S F H R S F A S E A V R I G T
GAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAA
241 -----+-----+-----+-----+-----+-----+-----+ 300
E G S P V K A Y L D I D E I I G A A K K
GTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCCTGTCTGAAAATGCCAGCTTGCC
301 -----+-----+-----+-----+-----+-----+-----+ 360
V K A D A I Y P G Y G F L S E N A Q L A
CGCGAGTGC GCGGAAAACGGCATTACTTTTATTGGCCCAACCCAGAGGTTCTTGATCTC
361 -----+-----+-----+-----+-----+-----+-----+ 420
R E C A E N G I T F I G P T P E V L D L
ACCGGTGATAAGTCTCGTGCGGTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTGGCG
421 -----+-----+-----+-----+-----+-----+-----+ 480
T G D K S R A V T A A K K A G L P V L A
GAATCCACCCCGAGCAAAAACATCGATGACATCGTTAAAAGCGCTGAAGGCCAGACTTAC
481 -----+-----+-----+-----+-----+-----+-----+ 540
E S T P S K N I D D I V K S A E G Q T Y
CCCATCTTTGTAAAGGCAGTTGCCGGTGGTGGCGGACGCGGTATGCGCTTTGTTTCTTCA
541 -----+-----+-----+-----+-----+-----+-----+ 600
P I F V K A V A G G G G R G M R F V S S
CCTGATGAGCTCCGCAAATTGGCAACAGAAGCATCTCGTGAAGCTGAAGCGGCATTCCGGC
601 -----+-----+-----+-----+-----+-----+-----+ 660
P D E L R K L A T E A S R E A E A A F G
GACGGTTCGGTATATGTGCAACGTGCTGTGATTAACCCCGAGCACATTGAAGTGCAGATC
661 -----+-----+-----+-----+-----+-----+-----+ 720
D G S V Y V E R A V I N P Q H I E V Q I

FIG. 1A

CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGT
721 -----+-----+-----+-----+-----+-----+ 780
L G D R T G E V V H L Y E R D C S L Q R
CGTCACCAAAAAGTTGTGCGAAATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGAT
781 -----+-----+-----+-----+-----+-----+ 840
R H Q K V V E I A P A Q H L D P E L R D
CGCATTTGTGCGGATGCAGTAAAGTTCTGCGCTCCATTGGTTACCAGGGCGCGGAACC
841 -----+-----+-----+-----+-----+-----+ 900
R I C A D A V K F C R S I G Y Q G A G T
GTGGAATTCTTGGTCGATGAAAAGGGCAACCACGTTTTTCATCGAAATGAACCCACGTATC
901 -----+-----+-----+-----+-----+-----+ 960
V E F L V D E K G N H V F I E M N P R I
CAGGTTGAGCACACCGTGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATG
961 -----+-----+-----+-----+-----+-----+ 1020
Q V E H T V T E E V T E V D L V K A Q M
CGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACC
1021 -----+-----+-----+-----+-----+-----+ 1080
R L A A G A T L K E L G L T Q D K I K T
CACGGTGCAGCACTGCAGTGCCGCATCACACGGAAGATCCAAACAACGGCTTCCGCCCA
1081 -----+-----+-----+-----+-----+-----+ 1140
H G A A L Q C R I T T E D P N N G F R P
GATACCGGAACATATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTTCGTCTTGACGGT
1141 -----+-----+-----+-----+-----+-----+ 1200
D T G T I T A Y R S P G G A G V R L D G
GCAGCTCAGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAAATGACC
1201 -----+-----+-----+-----+-----+-----+ 1260
A A Q L G G E I T A H F D S M L V K M T
TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCTCGTGACAGCGCGCTTGGCTGAGTTC
1261 -----+-----+-----+-----+-----+-----+ 1320
C R G S D F E T A V A R A Q R A L A E F
ACCGTGTCTGGTGTGCAACCAACATTGGTTTCTTTCGCTGCGTTGCTGCGGGAAGAGGAC
1321 -----+-----+-----+-----+-----+-----+ 1380
T V S G V A T N I G F L R A L L R E E D
TTCACTTCCAAGCGCATCGCCACCGGATTTATCGGCGATCACCCACACCTCCTTCAGGCT
1381 -----+-----+-----+-----+-----+-----+ 1440
F T S K R I A T G F I G D H P H L L Q A

FIG. 1B

1441 CCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC 1500
P P A D D E Q G R I L D Y L A D V T V N
1501 AAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCAATCGATAAGCTGCCCAACATC 1560
K P H G V R P K D V A A P I D K L P N I
1561 AAGGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCCAGCCGCG 1620
K D L P L P R G S R D R L K Q L G P A A
1621 TTTGCTCGTGATCTCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGAT 1680
F A R D L R E Q D A L A V T D T T F R D
1681 GCACACCAGTCTTTGCTTGCGACCCGAGTCCGCTCATTCGCACTGAAGCCTGCGGCAGAG 1740
A H Q S L L A T R V R S F A L K P A A E
1741 GCCGTCGCAAAGCTGACTCCTGAGCTTTTGTCCGTGGAGGCCTGGGGCGGCGGACCTAC 1800
A V A K L T F E L L S V E A W G G A T Y
1801 GATGTGGCGATGCGTTTCCTCTTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAG 1860
D V A M R F L F E D P W D R L D E L R E
1861 GCGATGCCGAATGTAAACATTCAGATGCTGCTTCGCGGCCGCAACACCGTGGGATAACAC 1920
A M P N V N I Q M L L R G R N T V G Y T
1921 CCGTACCCAGACTCCGTCTGCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGAC 1980
P Y P D S V C R A F V K E A A S S G V D
1981 ATCTTCCGCATCTTCGACGCGCTTAACGACGTCTCCAGATGCGTCCAGCAATCGACGCA 2040
I F R I F D A L N D V S Q M R P A I D A
2041 GTCCTGGAGACCAACACCGCGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCT 2100
V L E T N T A V A E V A M A Y S G D L S
2101 GATCCAAATGAAAAGCTCTACACCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC 2160
D P N E K L Y T L D Y Y L K M A E E I V
2161 AAGTCTGGCGCTCACATTCTGGCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCG 2220
K S G A H I L A I K D M A G L L R P A A

FIG. 1c

2221 GTAACCAAGCTGGTCACCGCACTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACC
-----+-----+-----+-----+-----+ 2280
V T K L V T A L R R E F D L P V H V H T
2281 CACGACACTGCGGGTGGCCAGTTGGCTACCTACTTTGCTGCAGCTCAAGCTGGTGCAGAT
-----+-----+-----+-----+-----+ 2340
H D T A G G Q L A T Y F A A A Q A G A D
2341 GCTGTTGACGGTGCTTCCGCACTGTCTGGCACCACCTCCCAGCCATCCCTGTCTGCC
-----+-----+-----+-----+-----+ 2400
A V D G A S A P L S G T T S Q P S L S A
2401 ATTGTTGCTGCATTCGCGCACACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCT
-----+-----+-----+-----+-----+ 2460
I V A A F A H T R R D T G L S L E A V S
2461 GACCTCGAGCCGTACTGGGAAGCTGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACC
-----+-----+-----+-----+-----+ 2520
D L E P Y W E A V R G L Y L P F E S G T
2521 CCAGGCCCAACCGGTCGCGTCTACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTG
-----+-----+-----+-----+-----+ 2580
P G P T G R V Y R H E I P G G Q L S N L
2581 CGTGCACAGGCCACCGCACTGGGCCTTGCTGATCGCTTCGAGCTCATCGAAGACAACCTAC
-----+-----+-----+-----+-----+ 2640
R A Q A T A L G L A D R F E L I E D N Y
2641 GCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTT
-----+-----+-----+-----+-----+ 2700
A A V N E M L G R P T K V T P S S K V V
2701 GGCGACCTCGCACTCCACCTGGTTGGTGCGGGTGTAGATCCAGCAGACTTTGCTGCAGAC
-----+-----+-----+-----+-----+ 2760
G D L A L H L V G A G V D P A D F A A D
2761 CCACAAAAGTACGACATCCCAGACTCTGTTCATCGCGTTCCCTGCGCGGCGAGCTTGGTAAC
-----+-----+-----+-----+-----+ 2820
P Q K Y D I P D S V I A F L R G E L G N
2821 CCTCCAGGTGGCTGGCCAGAACCCTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGC
-----+-----+-----+-----+-----+ 2880
P P G G W P E P L R T R A L E G R S E G
2881 AAGGCACCTCTGACGGAAGTTCTTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCC
-----+-----+-----+-----+-----+ 2940
K A P L T E V P E E E Q A H L D A D D S

FIG. 1D

2941 AAGGAACGTCGCAACAGCCTCAACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTC 3000
-----+-----+-----+-----+-----+-----+
K E R R N S L N R L L F P K P T E E F L
3001 GAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGA 3060
-----+-----+-----+-----+-----+-----+
E H R R R F G N T S A L D D R E F F Y G
3061 CTGGTTCGAGGGCCGCGAGACTTTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGT 3120
-----+-----+-----+-----+-----+-----+
L V E G R E T L I R L P D V R T P L L V
3121 CGCCTGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTC 3180
-----+-----+-----+-----+-----+-----+
R L D A I S E P D D K G M R N V V A N V
3181 AACGGCCAGATCCGCCCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTCAACCGCAACC 3240
-----+-----+-----+-----+-----+-----+
N G Q I R P M R V R D R S V E S V T A T
3241 GCAGAAAAGGCAGATTCTTCCAACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTGTC 3300
-----+-----+-----+-----+-----+-----+
A E K A D S S N K G H V A A P F A G V V
3301 ACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAG 3360
-----+-----+-----+-----+-----+-----+
T V T V A E G D E V K A G D A V A I I E
3361 GCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATTGAACGCGTTGTG 3420
-----+-----+-----+-----+-----+-----+
A M K M E A T I T A S V D G K I E R V V
3421 GTTCCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA 3474
-----+-----+-----+-----+-----+-----+
V P A A T K V E G G D L I V V V S *

FIG. 1E

| | | | | |
|--------------|-----|-----|---|-----|
| ATCC 21253 | pyc | 1 | | 50 |
| NRRL B-11474 | pyc | | MST HTSSTLPAPK KILVANRGEI AVRAFRAALE | |
| | | | MTAITLGGLL LKGIITLV | |
| ATCC 21253 | pyc | 51 | | 100 |
| NRRL B-11474 | pyc | | TGAATVAIYP REDRGSFHRS FASEAVRIGT EGSPVKAYLD IDEIIGAACK | |
| ATCC 21253 | pyc | 101 | | 150 |
| NRRL B-11474 | pyc | | VKADAIYPGY GFLSENAQLA RECAENGITF IGPTPEVLDDL TGDKSRVTA | |
| ATCC 21253 | pyc | 151 | | 200 |
| NRRL B-11474 | pyc | | AKKAGLPVLA ESTPSKNIDE IVKSAEGQTY PIFVKAVAGG GGRGMRFVAS | |
| | | | D | S |
| ATCC 21253 | pyc | 201 | | 250 |
| NRRL B-11474 | pyc | | PDELRLATE ASREAEAAFG DGAVYVERAV INPQHIEVQI LGDHTGEVVH | |
| | | | S | R |
| ATCC 21253 | pyc | 251 | | 300 |
| NRRL B-11474 | pyc | | LYERDCSLQR RHQKVVEIAP AQHLDPELRD RICADAVKFC RSIGYQGAGT | |
| ATCC 21253 | pyc | 301 | | 350 |
| NRRL B-11474 | pyc | | VEFLVDEKGN HVFIEMNPRI QVEHTVTEEV TEVDLVKAQM RLAAGATLKE | |
| ATCC 21253 | pyc | 351 | | 400 |
| NRRL B-11474 | pyc | | LGLTQDKIKT HGAALQCRIT TEDPNNGFRP DTGTITAYRS PGGAGVRLDG | |
| ATCC 21253 | pyc | 401 | | 450 |
| NRRL B-11474 | pyc | | AAQLGGEITA HFDSMLVKMT CRGSDFETAV ARAQRALAEF TVSGVATNIG | |
| ATCC 21253 | pyc | 451 | | 500 |
| NRRL B-11474 | pyc | | FLRALLREED FTSKRIATGF IADHPHLLQA PPADDEQGRI LDYLADVTVN | |
| | | | G | |
| ATCC 21253 | pyc | 501 | | 550 |
| NRRL B-11474 | pyc | | KPHGVRPKDV AAPIDKLPNI KDLPLPRGSR DRLKQLGPAA FARDLREQDA | |
| ATCC 21253 | pyc | 551 | | 600 |
| NRRL B-11474 | pyc | | LAVTDTTFRD AHQSLLATRV RSFALKPAAE AVAKLTPELL SVEAWGGATY | |
| ATCC 21253 | pyc | 601 | | 650 |
| NRRL B-11474 | pyc | | DVAMRFLFED PWDRLDELRE AMPNVNIQML LRGRNTVGYT PYPDSVCRAF | |
| ATCC 21253 | pyc | 651 | | 700 |
| NRRL B-11474 | pyc | | VKEAASSGVD IFRIFDALND VSQMRPAIDA VLETNTAVAE VAMAYSGDLS | |
| ATCC 21253 | pyc | 701 | | 750 |
| NRRL B-11474 | pyc | | DPNEKLYTLD YYLKMAEEIV KSGAHILAIAK DMAGLLRPAA VTKLVTAIRR | |
| ATCC 21253 | pyc | 751 | | 800 |
| NRRL B-11474 | pyc | | EFDLPVHVHT HDTAGGQLAT YFAAAQAGAD AVDGASAPLS GTTSQPSLSA | |

FIG. 2A

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| | | | |
|--------------|-----|--|------|
| ATCC 21253 | pyc | 801 | |
| NRRL B-11474 | pyc | IWAAPAHTRR DTGLSLEAVS DLEPYWEAVR GLYLPFESGT PGPTGRVYRH | 850 |
| ATCC 21253 | pyc | 851 | |
| NRRL B-11474 | pyc | EIPGGQLSNL RAQATALGLA DRFELIEDNY AAVNEMLGRP TKVTPSSKVV | 900 |
| ATCC 21253 | pyc | 901 | |
| NRRL B-11474 | pyc | GDLALHLVGA GVDPAADFAAD PQKYDIPDSV IAFRLRGELGN PPGGWPEPLR | 950 |
| ATCC 21253 | pyc | 951 | |
| NRRL B-11474 | pyc | TRALEGRSEG KAPLTEVPPEE EQAHL DADDS KERRNSLNRL LFPKPTEEF | 1000 |
| ATCC 21253 | pyc | 1001 | |
| NRRL B-11474 | pyc | EHRRRFGNTS ALDDREFFYG LVEGRETLIR LPDVRTPLL V RLD AISEPDD | 1050 |
| ATCC 21253 | pyc | 1051 | |
| NRRL B-11474 | pyc | KGMRNVVANV NGQIRPMRVR DRSVESVTAT AEKADSSNKG HVAAPFAGVV | 1100 |
| ATCC 21253 | pyc | 1101 | |
| NRRL B-11474 | pyc | TVTVAEGDEV KAGDAVAIIE AMKMEATITA SVDGKIDRVV VPAATKVEGG | 1150 |
| | | E | |
| ATCC 21253 | pyc | 1151 | |
| NRRL B-11474 | pyc | DLIVVVS | |

FIG. 2B

GTGACTGCTATCACCCCTTGGCGGTCTCTTGTGAAAGGAATAATTACTCTAGTGTGCGACTCACACATCTTC
AACGCTTCCAGCATTCAAAAAGATCTTGGTAGCAAACCGCGCGGAAATCGCGGTCCGTGCTTTCCTGTCAG
CACTCGAAACCGGTGCAGCCACGGTAGCTATTTACCCCGTGAAGATCGGGGATCATTCCACCGCTCTTTT
GCTTCTGAAGCTGTCCGCATTGGTACTGAAGGCTCACCAGTCAAGGCGTACCTGGACATCGATGAAATTAT
CGGTGCAGCTAAAAAAGTTAAAGCAGATGCTATTTACCCGGGATATGGCTTCTGTCTGAAAAATGCCAGC
TTGCCCGCGAGTCCGCGGAAAAACGGCATTACTTTTATTGGCCCAACCCAGAGGTTCTTGATCTCACCGGT
GATAAGTCTCGTGCGGTAACCGCGCGGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCGAGCAA
AAACATCGATGACATCGTTAAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTAAGGCAGTTGCCGGTG
GTGGCGGACGCGGTATGCGCTTTGTTTCTTACCTGATGAGTCCGCAAATTGGCAACAGAAGCATCTCGT
GAAGCTGAAGCGGCATTCCGCGACGGTTCGGTATATGTGCAACGTGCTGTGATTAACCCCGAGCACATTGA
AGTGCAGATCCTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACGTGACTGCTCACTGCAGCGTC
GTCACCAAAAAGTTGTGCAAAATTGCGCCAGCACAGCATTGGATCCAGAACTGCGTGATCGCATTGTGCG
GATGCAGTAAAGTTCTGCCGCTCCATTGGTTACCAGGGCGCGGGAACCGTGGAATTTTGGTTCGATGAAAA
GGGCAACCACGTTTTTCATCGAAATGAACCCACGTATCCAGTTGAGCACACCGTGACTGAAGAAGTCACCG
AGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACCTTGAAGGAATTGGGTCTGACCCAA
GATAAGATCAAGACCCACGGTGCAGCACTGCAGTGCCGCATCACCACGGAAGATCCAAACAACGGCTTCCG
CCCAGATACCGGAACTATCACCGCGTACCGCTCACCAGGCGGAGCTGGCGTTCTGTTGACGGTGCAGCTC
AGCTCGGTGGCGAAATCACCGCACACTTTGACTCCATGCTGGTGAAGTACCTGCCGTGGTTCGACTTT
GAAACTGCTGTTGCTCGTGACAGCGCGCTTGGCTGAGTTACCGTGTCTGGTGTGCAACCAACATTGG
TTTTCTTGCGTGCGTTGCTGCGGGAAGAGGACTTCACTTCCAAGCGCATCGCCACCGGATTTATCGGCGATC
ACCCACACCTCCTTCAGGCTCCACCTGCGGATGATGAGCAGGGACGCATCCTGGATTACTTGGCAGATGTC
ACCGTGAACAAGCCTCATGGTGTGCGTCCAAAGGATGTTGCAGCACCATCGATAAGCTGCCCAACATCAA
GGATCTGCCACTGCCACGCGGTTCCCGTGACCGCCTGAAGCAGCTTGGCCAGCCGCGTTTGCTCGTGATC
TCCGTGAGCAGGACGCACTGGCAGTTACTGATACCACCTTCCGCGATGCACACAGTCTTTGCTTGCGACC
CGAGTCCGCTCATTGCACTGAAGCCTGCGGCAGAGGCGCTCGCAAAGCTGACTCCTGAGCTTTTGTCCGT
GGAGGCCTGGGGCGGCGGACCTACGATGTGGCGATGCGTTTTCTCTTTGAGGATCCGTGGGACAGGCTCG
ACGAGCTGCGCGAGGCGATGCCGAATGTAACATTAGATGCTGCTTCGCGGCCGCAACACCGTGGGATAC
ACCCCGTACCCAGACTCCGTCTGCCGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGACATCTTCCG
CATCTTCGACGCGCTTAACGACGTCTCCAGATGCGTCCAGCAATCGACGCAGTCTTGAGACCAACACCG
CGGTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTACACCTGGAT
TACTACCTAAAGATGGCAGAGGAGATCGTCAAGTCTGGCGCTCACATTCTGGCCATTAAGGATATGGCTGG
TCTGCTTCGCCAGCTGCGGTAACCAAGCTGGTACCAGCACTGCGCGTGAATTGATCTGCCAGTGCACG
TGCACACCCAGACACTGCGGGTGGCCAGTTGGCTACCTACTTTGCTGCAGCTCAAGCTGGTGCAGATGCT
GTTGACGGTGCTTCCGCACCACTGTCTGGCACCACCTCCAGCCATCCCTGTCTGCCATTGTTGCTGCATT
CGCGCACACCCGTGCGATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAAGCTG
TGCGCGGACTGTACCTGCCATTTGAGTCTGGAACCCAGGCCCAACCGGTGCGGTCTACCGCCAGAAATC
CCAGGCGGACAGTTGTCCAACCTGCGTGACAGGCCACCGCACTGGGCTTGTCTGATCGCTTCGAGCTCAT
CGAAGACAACCTACGCAGCCGTTAATGAGATGCTGGGACGCCCAACCAAGGTACCCCATCTCCAAGGTTG
TTGGCGACCTCGCACTCCACCTGGTTGGTGGCGGTGTAGATCCAGCAGACTTTGCTGCAGACCCACAAAAG
TACGACATCCAGACTCTGTATCGCGTTCTGCGCGGCGAGCTTGGTAACCTCCAGGTGGCTGGCCAGA
ACCACTGCGCACCCGCGCACTGGAAGGCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTTCTGAGGAAG
AGCAGGCGCACCTCGACGTGATGATTCCAAGGAACGTGCAACAGCCTCAACCGCTGCTGTTCCGAAG
CCAACCGAAGAGTTCTCGAGCACCGTCGCCGCTTCGGCAACACCTCTGCGCTGGATGATCGTGAATTCTT
CTACGGAAGTGGTTCGAGGGCCGCGAGACTTTGATCCGCTGCCAGATGTGCGCACCCCACTGCTTGTTCGCC
TGGATGCGATCTCTGAGCCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGC
CCAATGCGTGTGCGTGACCGCTCCGTTGAGTCTGTACCAGCAACCGCAGAAAAGGCAGATTCTCCAACAA
GGGCCATGTTGCTGCACCATTCGCTGGTGTGTCACTGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTG
GAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACAATCACTGCTTCTGTTGACGGCAAGATT
GAACGCGTTGTGGTTCTGCTGCAACGAAGGTGGAAGGTGGCGACTTGATCGTCTGCTGTTCTCTAA

FIG.3A

MTAITLGGLLLKGIITLVSTHTSSTLPFAFKILVANRGEIAVRAFRAALETGAATVAIYPREDRGSFHRSFASEAVRIG
TEGSPVKAYLDIDEIIGAACKVKADAIYPGYGFLSENAQLARECAENGITFIGPTPEVLDLTGDKSRAVTAACKAGLPV
LAESTPSKNIDDIVKSAEGQTYPIFVKAVAGGGGRGMRFVSSPDELRLKATEASREAEAAFDDGSVYVERAVINPQHIE
VQILGDRTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIE
NPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKEGLTQDKIKTHGAALQCRIITTEDPNNGFRPDTGTITAYRSPGGAG
VRLDGAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDH
PHLLQAPPADDEQGRILDYLDVTVNKPVGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLKQLGPAAFARDLREQDALAV
TDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQMLLR
GRNTVGYTPYPDSVCRAVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDY
YLKMAEEIVKSGAHLAIKDMAGLLRPAAVTKLVLTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASAPLS
GTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSNLRAQATALGL
ADRFELIEDNYAAVNEMLRPTKVTTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGWPEP
LRTRALEGRSEGKAPL TEVPEEEQAHL DADDSKERRNSLNRLLPKPTEEFLEHRRRFGNTSALDDREFFYGLVEGRET
LIRLPDVRTPLLVRDAISEPDDKGMNRNVANVNGQIRPMRVDRSVESVTATAEKADSSNKGHVAAPFAGVVTVTVAE
GDEVKAGDAVAII EAMKMEATITASVDGKIERVVVPAATKVEGGDLIVVVS

FIG.3B

EFFECT OF VARIOUS SUBSTRATE CONCENTRATIONS ON PYRUVATE CARBOXYLASE
ACTIVITY FROM *C. glutamicum* BF100 (○) AND ATCC 21253 (●).

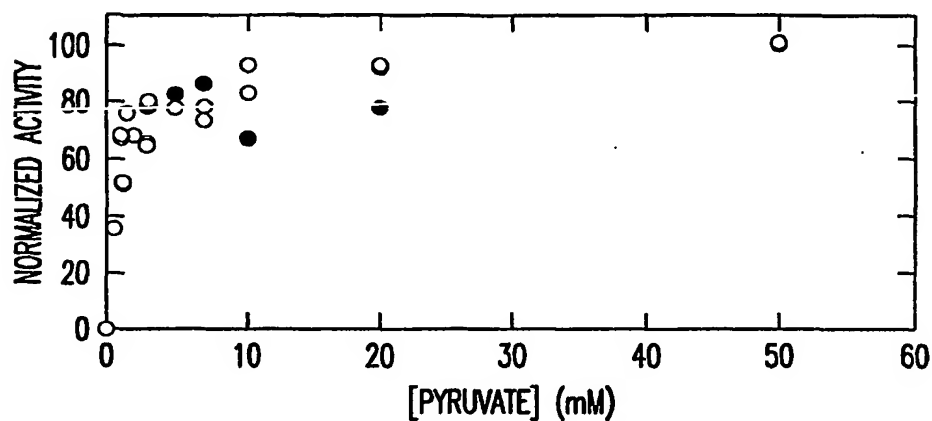


FIG. 4A

EFFECT OF VARIOUS SUBSTRATE CONCENTRATIONS ON PYRUVATE CARBOXYLASE
ACTIVITY FROM *C. glutamicum* BF100 (○) AND ATCC 21253 (●).

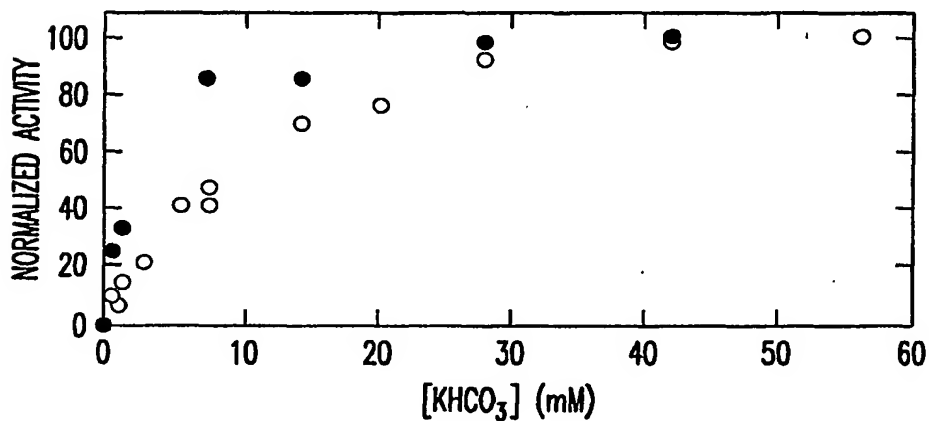


FIG. 4B

EFFECT OF VARIOUS SUBSTRATE CONCENTRATIONS ON PYRUVATE CARBOXYLASE
ACTIVITY FROM *C. glutamicum* BF100 (○) AND ATCC 21253 (●).

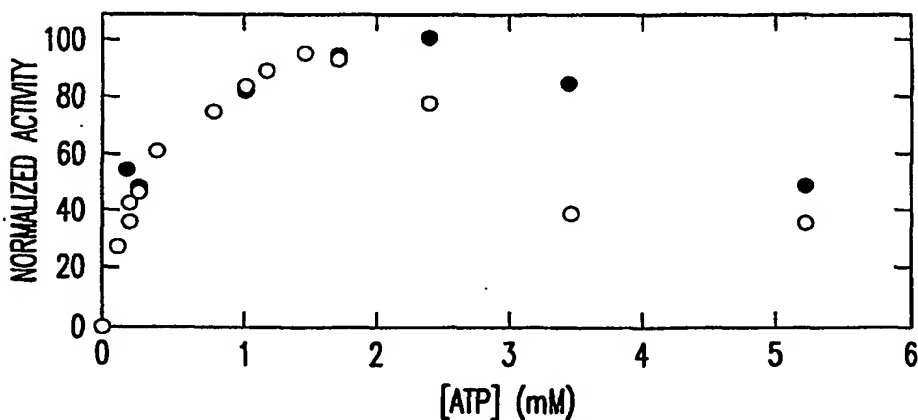


FIG. 4C

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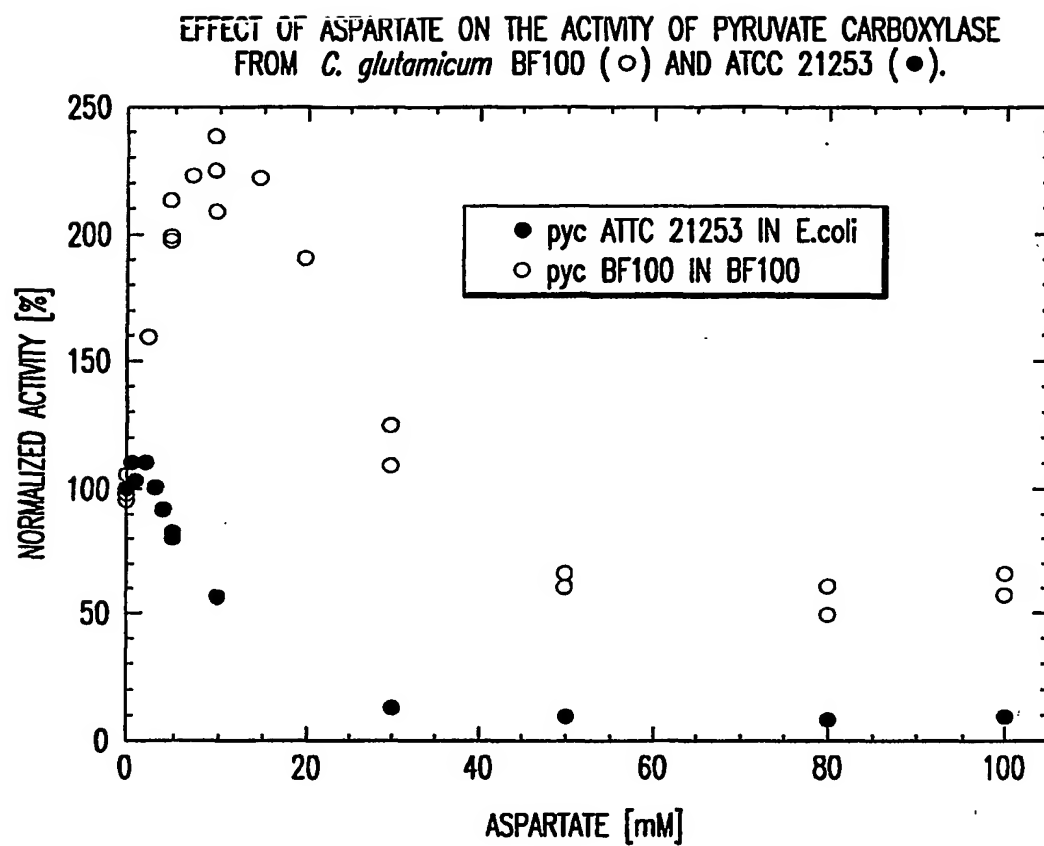


FIG. 5

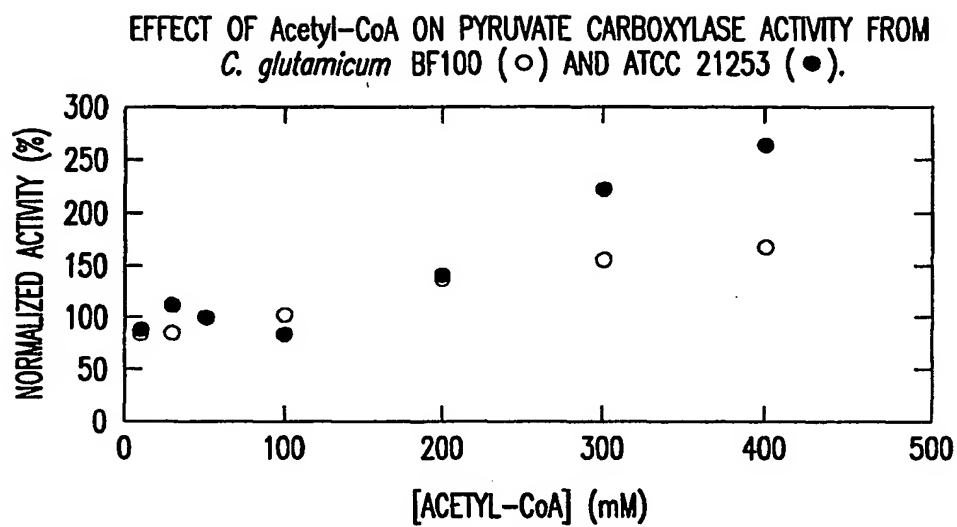


FIG. 6

Applicant's or agent's file
reference number 1533.123PC01

International application No.
TBA

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 12 line 12.

B. IDENTIFICATION OF DEPOSIT

Further deposits are identified on an additional sheet ☐

Name of depository institution

AGRICULTURAL RESEARCH SERVICE CULTURE COLLECTION (NRRL)

Address of depository institution (including postal code and country)

1815 North University Street
Peoria, Illinois 61604
United States of America

Date of deposit
30 May 2000 (30.05.00)

Accession Number
NRRL B-30293

C. ADDITIONAL INDICATIONS (leave blank if not applicable)

This information is continued on an additional sheet ☐

Escherichia coli DH5 α MCR pBSII-PYCBF100

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)

E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)

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